

NO: 10) and MREIVHI (SEQ ID NO: 11). These two sequences differed only by three amino acids (VIS instead of IVH). Comparison of the two sequence with known protein sequences using FastA protein search engine, showed the latter sequences to encode the first seven N-terminal amino acids of α - and β -tubulins. The identification of tubulins, as the 57 kDa protein was consistent with the apparent molecular mass and the potential degradation products that were observed following long incubation periods. To further confirm the identity of the 57 kDa protein as tubulins, Western blot analysis was performed on hexapeptide-bound 57 kDa protein and total cell lysate resolved by SDS-PAGE and transferred to nitrocellulose membrane. The nitrocellulose membrane was then probed with anti α -tubulin and anti- β -tubulin monoclonal antibodies, respectively. Figure 14 shows the results of the Western blot analysis. Consistent with the sequencing results, both tubulin subunits (α and β) were recognized in the lanes containing the hexapeptide bound proteins. Thus, establishing the identity of the 57 kDa protein as α and β -tubulin.

Please delete the paragraph on page 22, lines 14-20 and replace it with the following paragraph:

Figure 10 shows the sequence alignment of three binding regions of HP-gp1 and HP-gp3 linker domains. Alignment of HP-gp1 (SEQ ID NO: 15) and HP-gp3 (SEQ ID NO: 14) linker domains is shown using a single-letter code for amino acids. The regions of high binding affinities for HP-gp3 and HP-gp1 are shown in bold. Identical amino acids are shown by single letter code between the two aligned sequences. Conserved amino acids are indicated by plus (+) sign. The numbers on each side of the amino acid sequence of the linker domains refer to the amino acid sequence of human P-gp1 and 3 as in (90, 111).

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Please delete the paragraph on page ²³25, lines ¹⁵⁻¹⁸47 and replace it with the following paragraph:

Figure 15 shows the helical wheel presentations of the high affinity binding region of HP-gp1 and HP-gp3 linker domains. The single-letter amino acid code for the high affinity binding region of HP-gp1 (SEQ ID NO: 12) and HP-gp3 (SEQ ID NO: 13) linker domains are shown. The positively charged amino acids on one side of the helix have been circled.